ISSN 0258-7122
Bangladesh J. Agril. Res. 35(1) : 95-100, March 2010

ESTIMATE OF GENETIC DIVERSITY IN SNAKE GOURD *(Trichosanthes cucumerina)*

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Abstract

The present investigation was conducted at the field and laboratory of the Department of Horticulture, Bangladesh Agricultural University, Mymensingh during the period from April 2004 to September 2004 to study the nature and magnitude of genetic diversity of 38 snake gourd genotypes collected from different regions of the country. Based on D^2 analysis, the genotypes were grouped into four different clusters, where the cluster I possessed maximum number (21) of genotypes followed by the cluster 11(8), III (7), and IV (2). Clustering pattern revealed that geographical diversity was not associated with genetic diversity i.e., genotypes collected from same location were grouped into different clusters. The maximum inter-cluster distance was observed between the clusters III and IV and that of minimum in between the clusters I and II. In case of intra-cluster distance, the maximum distance was observed in the cluster IV and that of minimum was observed in the cluster III. Considering cluster mean, the genotypes of cluster IV could be selected for yield per plant and other yield contributing characters.

Keywords: Cluster, D^2 analysis, genetic diversity, snake gourd *(Trichosanthes cucumerina).*

Introduction

Snake gourd *(Trichosanthes cucumerina)* belongs to the family Cucurbitaceae and it is an important summer vegetable in Bangladesh, but it may grow throughout the year except extreme winter. It is a popular vegetable with moderately high nutritive value. The total production of snake gourd during 2003-2004 was 136000 tons on the area of 1,59,000 acres of land (BBS, 2004). This figure indicates the low yield potentiality of our cultivars. Among many reasons, the lack of high yielding variety is one of the reasons for low yield of this crop in Bangladesh.

In crop improvement programme, genetic diversity has been considered as an important factor which is also essential pre-requisite for hybridization programme for obtaining progenies with important desirable characters like disease resistance, earliness, quality or even performance of a particular character (Chowdhury *et al.,* 1975). For the yield improvement and future utilization of local germplasm, genetic diversity of bitter gourd (Kundu, 2008) and snake

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gourd (Ahmed *et al.*, 2000 and Rahman, 2004) was estimated at Bangabandhu Sheikh Mujibur Rahman Agril. University (BSMRAU) Bangladesh. According to Ahmed *et al.* (2000), there has been a great scope for genetic improvement of snake gourd as there is a wide range of variability exists in Bangladesh. Genetically diverse and geographically isolated lines may generate a wide range of variation when brought together. Knowledge of genetic diversity among existing cultivars of any crop is essential for long- term success in breeding programme and to maximize the exploitation of the germplasm resources (Belaj *et al.*, 2002). Because, it provides us about the relationship among elite breeding population and helps in selecting desirable parents for establishing new breeding population. Therefore, information on its genetic architecture is essential. Under such circumstances, this study was conducted to assess the genetic diversity present in the collected snake gourd germplasm.

Materials and Method

Thirty eight genotypes of snake gourd collected under the USDA funded project entitled "Collection, Evaluation, Conservation and Utilization of Landraces and Wild relatives of some Important Vegetables and Fruits of Bangladesh (CVFB)" from different parts of the country were grown in the field following RCBD with three replications during the period from April 2004 to September 2004. One genotype represented one treatment and three plants of a genotype represented one replication. After final land preparation, pits of 50 x 50 × 30 cm were prepared in each block with the spacing of 2 × 1.5 m. Each block was 32 m × 5 m in size. Seven-day seedling raised in poly bag, were then transplanted in the pit. Fertilizers of 5 tons cowdung, 125 kg urea, 80 kg TSP, and 60 kg MP, 80 kg gypsum, and 6 kg borax per hectare were applied (Anonymous, 1991). Half of the cowdung, TSP, MP, gypsum, and borax were applied at the time of land preparation and rests were applied in the pit. Plants were supported by trellis and other intercultural operations, such as weeding, irrigation, plant protection measures, etc. were done as and when needed. Observations were taken on whole plot basis for seven yield and yield contributing characters. The characters were sex ratio, node number for first female flowering, number of fruits per plant, number of seeds per fruit, average fruit weight, fruit length, and yield per plant. The analyses of variance and covariance were done for selected characters for divergence studies. Genetic diversity was worked out following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952) to clustering in Tocher's method.

Results and Discussion

Clustering of genotypes

Genetic divergence among the genotypes of snake gourd was studied through Mohalanobis's D^2 analysis. By application of non-hierarchical clustering using

covariance matrix, 38 genotypes were grouped into four different clusters (Table 1). The cluster I possessed maximum number of genotypes (21) followed by the cluster 11(8), III (7), and IV (2).

Table 1. Distribution of 38 genotypes of snake gourd in different clusters.

Clusters	Number of genotypes with percent in each cluster	Genotypes with collection site
1	21(55.26%)	TA 0I (Jamalpur), TA 06 (Mymensingh), TAIl (Pabna), TA 12 (Mymensingh), TA 16 (Tangail), TA 22 (Mymensingh), TA 31, TA 37, TA 39 and TA 40 (Comilla), TA 48 (Patuakhali), TA 50 (Khagrachari Hill tract), TA 51 and TA 52 (Mymensingh), TA 56 (Kushtia), TA 59 (Dinajpur), TA 60 (Manikganj), TA 62 (Dinajpur), TA 64 (Chittagong), TA 65 and TA 67 (Mymensingh)
11	8 (21.05%)	TA 08 and TA 20 (Mymensingh), TA 34 (Comilla), TA 44 (Chittagong), TA 49 (Khatrachari Hill Tract), TA 55 (Joypurhat), TA 57 (Dinajpur), TA 6I (Manikganj)
III	7 (18.42%)	TA 05 (Mymensingh), TA 15 (Pabna), TA 17 (Tangail), TA 19 (Pabna), TA 35 (Comilla), TA 43 (Chittagong), TA 53 (Khagrachari Hill Tract)
IV	2 (5.26%)	TA 21 (Mymensingh), TA 42 (Chittagong)

It is interesting to note that 55.26% of the genotypes were included in the cluster 1, followed by cluster 11(21.05%), III (18.42%), and IV (5.26%), respectively (Table 1). Clustering pattern of the genotypes revealed that the genotype collected from the same region did not fall in a single cluster. As for example, 4 genotypes collected from Chittagong District were grouped into four different clusters (I, II, III, and IV), showing TA 42 in cluster IV, TA 43 in cluster III, TA 44 in cluster II, and TA 64 in cluster I. Similarly, eleven genotypes collected from Mymensingh District were distributed into different four clusters (cluster I, II, III, and IV) (Table 1). This result indicated that factors other than geographical separation are also responsible for divergence, and the genotypes that have originated from the same place may have different genetic architecture. The present findings also are in agreement with Rashid (2000) in pumpkin, Banik (2003) and Rahman (2004) in snake gourd. Lack of free relationship between geographical and genetic diversity was also explained by Upadhya and Murty (1970), who explained that genetic drift and natural selection in different environments can cause high diversity among genotypes.

Intra and inter-cluster distance

The intra-cluster distance was highest in the cluster IV followed by the cluster I, II, and III (Fig. 1). The minimum intra-cluster distance was observed in the cluster III, which included seven genotypes. The inter-cluster D^2 values varied from 457.75 to 8883.89 indicating wide diversity among the genotypes. The inter-cluster distance was the highest between the cluster III, and IV followed by the distance between I and IV, II and IV, II and III, and I and III. The genotypes grouped in the clusters III and IV that showed maximum inter-cluster distance are expected to obtain high heterosis in hybridization and to show wide variability in genetic make-up. The lowest inter-cluster distance that was observed in the cluster I and II suggests that genotypes of these clusters had closeness among themselves (Table 2 & Fig. 1).

Table 2. Average intra and inter cluster distances (D^2) for 38 snake gourd genotypes.

Clusters	I	II	III	IV
I	**412.73** (20.32)	457.75 (21.32)	1016.44 (31.88)	5380.33 (73.35)
II		**406.25** (20.16)	1044.85 (32.32)	1510.83 (38.87)
III			**192.93** (13.89)	8883.89 (94.25)
IV				**713.95** (26.72)

D = $\sqrt{D^2}$ (indicated within parenthesis); Underline bold figures indicated intra cluster distance

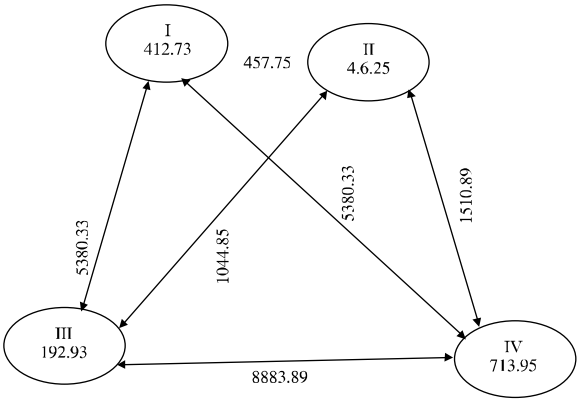

Fig I. Cluster diagram showing the average intra and inter cluster distances (D= $\sqrt{D^2}$) of snake gourd genotypes.

Note: The values along the lines indicate inter cluster distances and the values within the circle indicate intra cluster distances.

Medium inter-cluster distances were observed between the cluster II and III, II and IV, I and III. It is mentioned that the crosses involving parents belonging to medium divergent clusters may also exhibit significant and positive heterosis (Karim and Mian, 2001 and Mian and Bhal, 1989). In this experiment, inter-cluster distance was always higher than intra-cluster distance. Sidhu and Gautom (1985) also found similar result in watermelon.

Cluster mean

Mean performance of different clusters for seven characters are shown in the Table 3. Although the cluster I had the maximum number of genotypes (21), remarkable feature was found in this cluster for different characters. The cluster I included the genotypes that produced larger number of fruits per plant though it was highest in cluster II. Genotypes belonging to the cluster III also contained highest mean value of sex ratio. However, smallest mean value of fruits per plant, node number for first female flowering, number of seeds per fruit, average fruit weight, and yield per plant were observed in the cluster III which might be due to the lowest performing genotypes. The cluster IV included the genotypes that produced highest mean for length of fruit, node number for first female flowering, number of seeds per plant, average fruit weight and yield per plant. But the genotypes belonging to the cluster IV showed the lowest sex ratio (male: female). Yield is the ultimate goal of any crop production. The genotypes belonging to the cluster IV were high yielding and therefore, this cluster ranked first in terms of yield per plant. Next position was held by the cluster II, then after the cluster I and lastly the cluster III (Table 3). Wide range of genetic divergence was noticed among the studied genotypes of snake gourd, and this divergence of the genotypes may be taken into account for selecting the parents for hybridization and future improvement programme of this crop through breeding.

Table 3. Cluster means for important yield contributing characters in 38 snake gourd genotypes.

Characters	Cluster mean			
	I	II	III	IV
Length of fruit (cm)	25.50	30.39	18.46	31.65
Sex ratio	25.31	22.85	27.21	15.99
Node no. for first female flowering	19.48	20.12	18.24	21.17
Number of ruits per pant	12.44	15.79	9.49	15.00
Number of seeds per fruit	41.21	44.39	31.54	50.83
Average fruit weight (g)	77.36	120.84	51.15	155.62
Yield per plant (kg)	0.96	1.91	0.49	2.29

Acknowledgements

The authors wish to acknowledge the authorities of CVFB Project, Department of Horticulture, BAU, Mymensingh for providing experimental materials and necessary supports to conduct the present study.

References

Ahmed, M.S., M.G. Rasul, M.K. Bashar, A.S.M. Mian. 2000. Variability and heterosis in snake gourd. *(Trichosanthes anguina* L.). *Bangladesh J. P1. Breed. Genet.*, **13**(1): 27-32.

Anonymous, 1991. Basat Barita Sabji, Utpadan, (in Bengali), BARI, Gazipur, Bangladesh. p. 239.

Banik, B.R. 2003. Inheritance pattern in snake gourd *(Trichosanthes anguina* L.). Ph.D Thesis. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rabman Agricultural University, Salna, Gazipur. pp. 1-60.

BBS. 2004. Monthly Statistical Bulletin, Bangladesh (October). Bangladesh Bureau of Statistics, Statistics Division, Ministry of Planning, Government of the People's Republic of Bangladesh, p. 52.

Belaj, A., Z. Satovic, L. Rallo and Trujillo. 2002. Genetic diversity and relationship in olive *(Olea europea* L) germplasm collection as determined by RAPD. *Theor. Appi. Genet.* **105**(4): 638-644.

Choudhury, B.D., P.N. Bhat and V.P. Singh, 1975. Genetic diversity in cluster beans. *Indian. J. Agric. Sci.*, **45:** 530-535.

Karim, M.S., M. Ali and M. A. K. Mian. 2001. Heterosis in ash gourd *(Benincasa hispida* Thumb. Cogn.). *Bangladesh J. P1. Breed Genet.* **14** (1): 2 1-28.

Kundu, *B.C.* 2008. Morpho-biochemical diversity and heterosis in bitter gourd *(Momordica charantia* L.). Ph.D. Dissertation. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur..

Mahalanobis, P.C. 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci. India, **2:**49-55.

Mian, M.A.K. and P.N. Bhal. 1989. Genetic divergence and hybrid performance in chickpea. *Indian J. Genet.* **40**(1): 119-129.

Rahman, A.K.M. .M. 2004. Genotype-Environment interaction, heterosis and sex modification in snake gourd *(Thichosanthes anguina* L.). Ph.D. Dissertation,. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur..

Rao, C. R. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York. pp. 45-110.

Rashid, M.M. 2000. Genetic divergence in pumpkin. MS Thesis. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. p 85.

Sidhu, A.S. and N.C. Gautom. 1985. Genetic divergence and hybrid performance in water melon. *Indian J. Agril. Sci.* **55:** 459-461.

Upadhya, M.R. and B.R. Murty. 1970. Genetic diversity in relation to geographical distribution in pear millet. *J. Plant Breed. Genet.* **75**(3&4): 125-128.